

Genomic map and GC content plots for the 101G10 and 60A5 clones. The top panel shows the 101G10 clone with a genomic map above a GC content plot. The map includes genes like CSAT, HYF1, ORF1, ORF2, ORF3, ORF4, TDM, THF, POC, DEAM, PTI, REP, ORF5, and MZTH. The GC content plot for 101G10 shows a baseline around 60% GC with several peaks and troughs. The bottom panel shows the 60A5 clone with a similar genomic map and GC content plot. The GC content plot for 60A5 shows a similar pattern to 101G10 but with some differences in peak heights and positions. A scale bar for % DNA Identity is provided between the two plots, ranging from >70 to >99.

Figure 2

Gene	Strain	TATA Box	Coding Start	TATA to Start (bp)
81 Hypoth 03	A	AAGCTAGACT TTTAAT TGGG ATCCGGCGGG GCGGCGCATG	-----	25
82	B	AAGCTAAACT TTTAAT TGGG ATCCGGCGGAG CCGGCGCGTG	-----	
83 Hypoth 02	A	GGAAACTTTG ATTATA CGGG CGTGCTGCCC CCGGGCCCAT G-----	-----	26
84	B	GGAAACTTTG ATTATA CGGG CGTACATTCC CCGGGCCCAT G-----	-----	
85 ORF 02	A	AAGGCAAGGT AATAAT AGCC TGCCGTCTGT AACGGCCGTA TG-----	-----	27
86	B	ACGGCAAGGT AATAAT AGCC TGCCGTCCGT ACCTGCCGTA TG-----	-----	
87 ORF 03	A	CATGGAAC TA GATATT AACC GGTTCGCGG ATCCCATGCA TG-----	-----	27
88	B	CATGGAAC TA GATAAT AACC GGTCCCGCG GTACAATGCA TG-----	-----	
89 PPI	A	ATACCGAGAA GTTATA GCAG GGTATGGAAT GTGCGCGCGC ATG-----	-----	28
90	B	AGCAGGACAA GTTATA GCAG GGTACAAAGG AGCAGCGCAC ATG-----	-----	
91 GSAT	A	ATCCGCCCTG ATTAAA TTAT GGGGGGAGCG GCCTGCTGCC GTG-----	-----	28
92	B	ATCCGCCCTC ATTAAA TTAC GGGGGGTACA ACCTGCTGCC GTG-----	-----	
93 ORF 05	A	CCTTCATACA CATAAA TCCC GCTTGGATGT GCGGCTGCGC ATG-----	-----	28
94	B	ACTTCATACA CATAAA TCCC GCTGAAACGG TCGTCCGCGC ATG-----	-----	
95 deaminase	A	.GGCATATAC CATAAT ATGC CGGGCGGTGG CACCATGGCC GTTG-----	-----	29
96	B	CCGCATATAC CATAAT ATGC CGGGCGGGGG CAGGCTGCCC .GTG-----	-----	
97 RNA helic	A	TGTACGAAAC CATAAA ACAA CAGGCCGCGT CAGGGCCGCG CGTG-----	-----	29
98	B	GGGTAGAAAC CATAAA ACAA CAGGCCGCGG CAGGGCG.CG CGTG-----	-----	
99 ORF 06	A	.ACACGCAG TATAAA CGGG GGCCCCGGCG GCGCGTATCA CATG-----	-----	29
100	B	ATACACGTGG TATAAA CAGA GG.CCGGACG GCGCGGACCA CATG-----	-----	
101 tRNA-tyr	A	GCGATAGTTA TTTAAA ACTA GGATGCCGAT CACGGATCGT CCCA-----	-----	29
102	B	GCGATAGTTA TTTAAA ACTA GGATGCCGGG CACCCGTCGT CCCA-----	-----	
103 TBP	A	CCGGGCCCCG GTTAAA ATAG CG.CACGGGC GGATCCTGAC CAATG-----	-----	30
104	B	CCGGGCCCCG GTTAAA ATAG AGTGCGGCCG GGCACCGGAT CAATG-----	-----	
105 TIM	A	GCGTCGATAG AATAAA TACG CGCAGGGGGC CCCGTGGCGC GATCGCCCGT G-----	-----	36
106	B	GCGTCGATAG AATAAA TACG CGC.GGGGCC GCGGTGC... GATCGCCCGT G-----	-----	
107 Hypoth 01	A	ATTTCAACTA CATAAA TGCC TAGTTACGCA GAAATAGCAA ACGACGTACT TCGACTAATG		45
108	B	ACTTCAACTA CATAAA TGCC TAGCTACGCA GAAATATCAA ACAAAGTACT TCGACTAATG		
109 ORF 01	A	ACGGCAGGCT ATTATT ACCT TGCCCTTGCCT TGTA ///.G CGGGGTGCGG CAGGGGATG		52
110	B	ACGGCAGGCT ATTATT ACCT TGCCGTGTG. TACA ///.G AGGGGGCCTG CCGGGAGTG		
111 Methylase	A	CTACAACGAT TTTAAG TCGG CGCCGGGGCA GCCG.///.G ATGTGGGGCA GGCAACATG		104
112	B	CTACAAAGAT TTTAAG ACGG CGCGGGTGCC GCCG.///.T GGCACGGGG CCTATCTTG		
113 16S RNA	A	TCCGCCGATGG TTTATA TGCC CATGGACGGG CCGATCCGAT CGTACGTGAC GC.///.AAT		220
114	B	CCGGCGATGG TTTATA TGCC CATGGACAAG GCGATCCGAT CGTACGTGAC GC.///.AAT		

Archaeal promoter
consensus

YTTAWA

10027305-042202

202210-908/2001

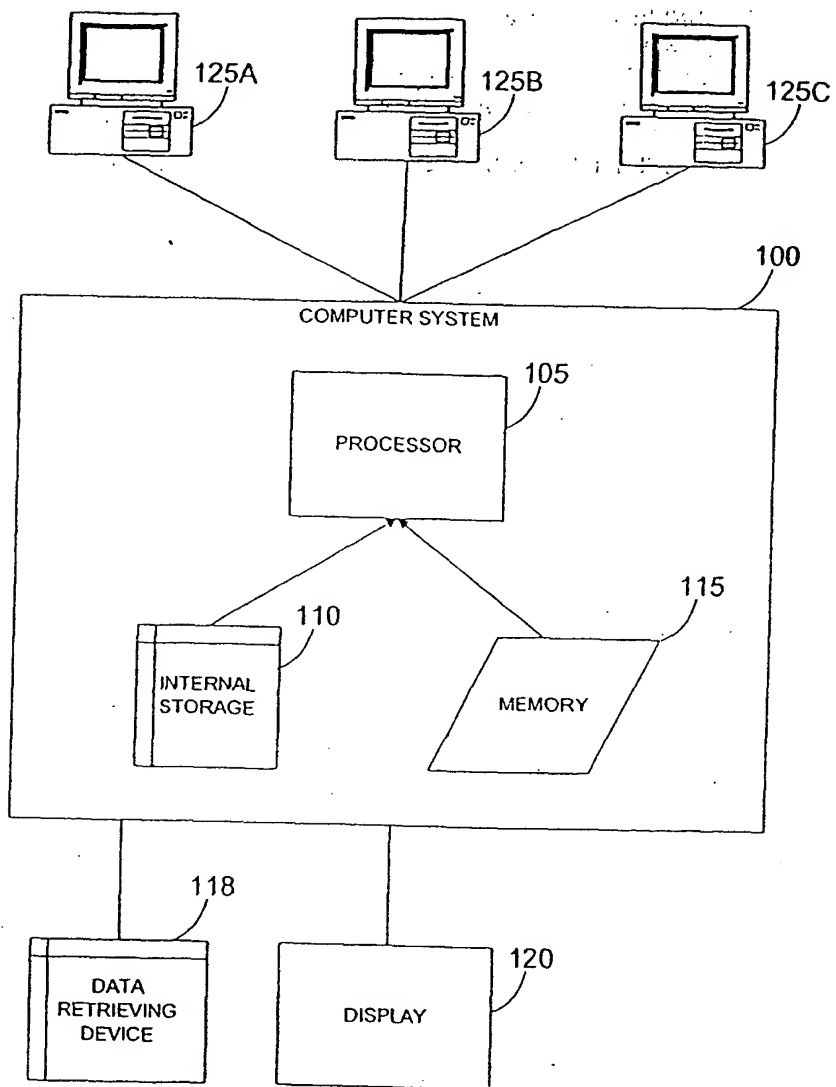


FIGURE 3

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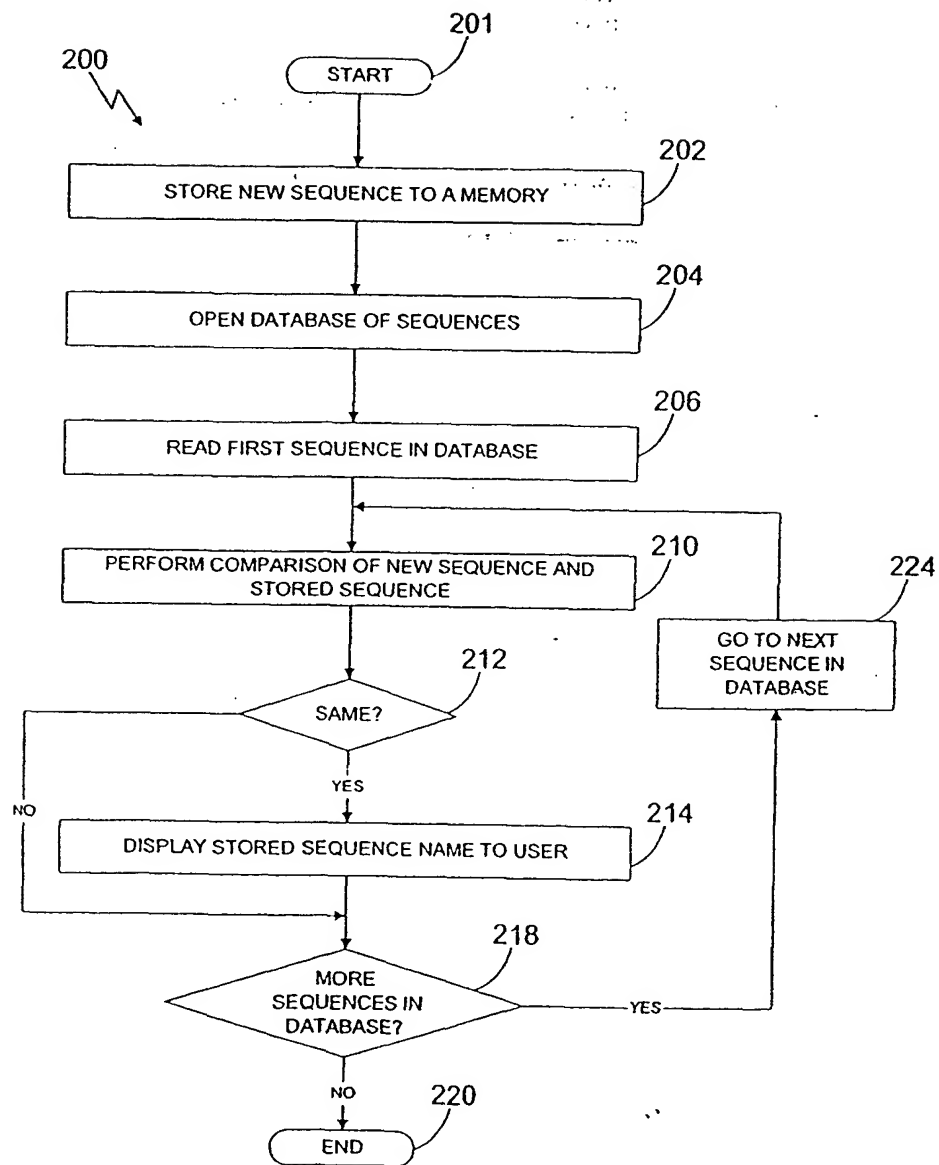


FIGURE 4

202240-9082001

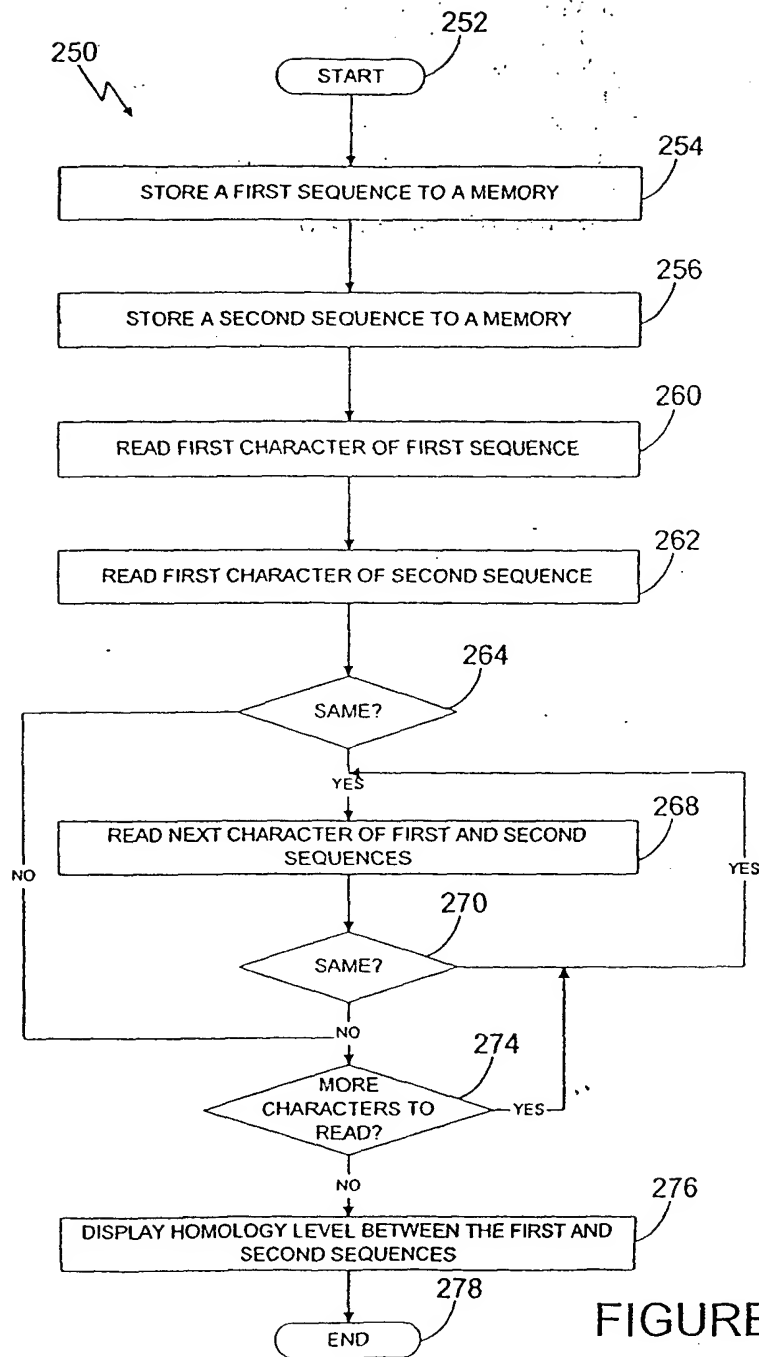


FIGURE 5

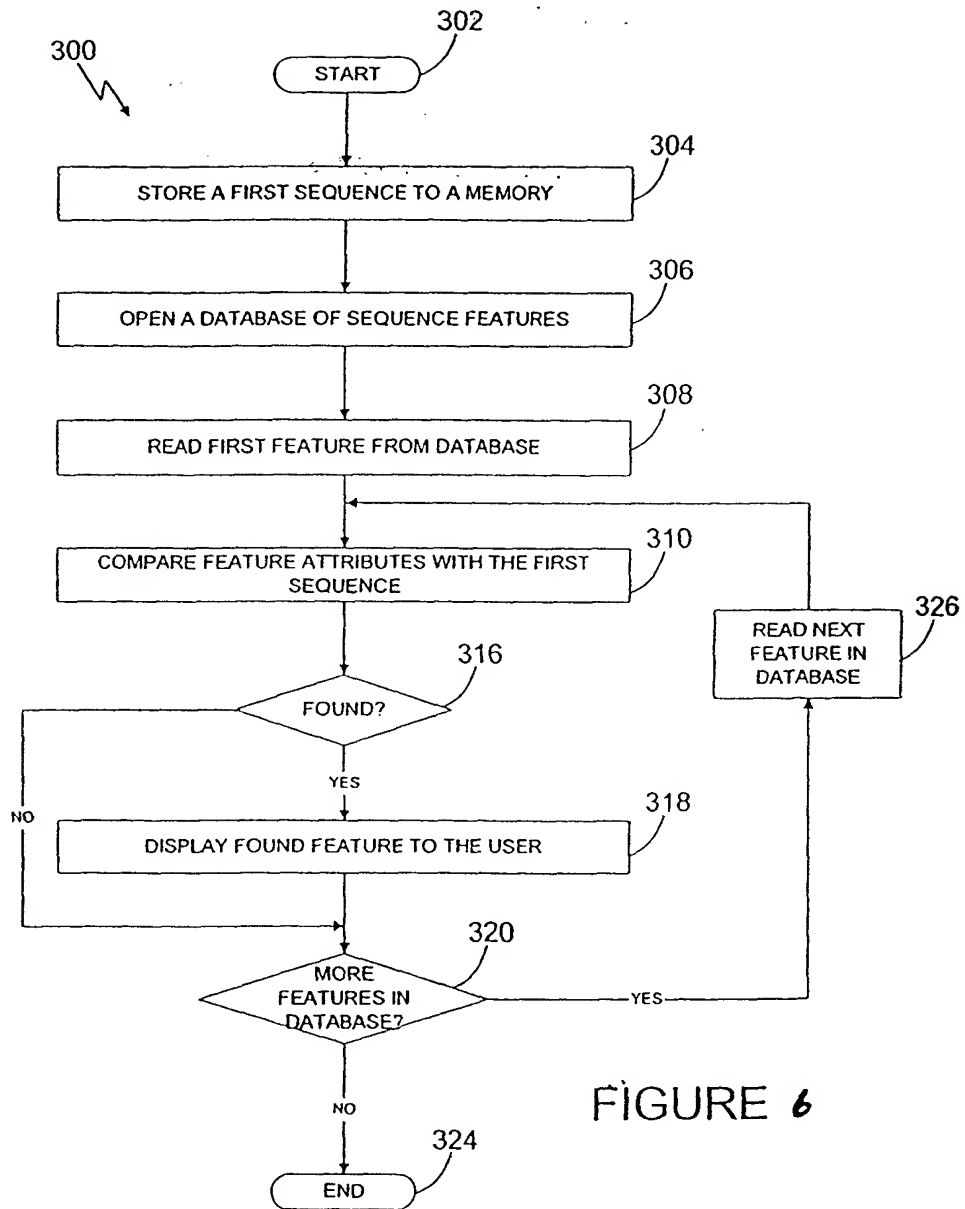


FIGURE 6